

SEQUENCE LISTING

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<120> Flt4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Therapy

<130> 28113/34891

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<151> 1997-07-28

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<151> 1992-10-09

<160> 22

<170> PatentIn Ver. 2.0

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atg acc cca acg acc tac aaa ggc tct gtg gac aac cag aca gac agt	3844
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1295

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Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro Tyr Cys Lys Val Leu
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Leu Leu His Glu Val His Ala Asn Asp Thr Gly Ser Tyr Val Cys Tyr
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Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr Thr Ala Ala Ser Ser
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130 135 140

Thr Leu Leu Val Asn Arg Lys Asp Ala Met Trp Val Pro Cys Leu Val
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Ser Ile Pro Gly Leu Asn Val Thr Leu Arg Ser Gln Ser Ser Val Leu
165 170 175

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Thr	Gly	Asn	Glu	Leu	Tyr	Asp	Ile	Gln	Leu	Leu	Pro	Arg	Lys	Ser	Leu	225	230	235	240
Glu	Leu	Leu	Val	Gly	Glu	Lys	Leu	Val	Leu	Asn	Cys	Thr	Val	Trp	Ala	245	250	255	
Glu	Phe	Asn	Ser	Gly	Val	Thr	Phe	Asp	Trp	Asp	Tyr	Pro	Gly	Lys	Gln	260	265	270	
Ala	Glu	Arg	Gly	Lys	Trp	Val	Pro	Glu	Arg	Arg	Ser	Gln	Gln	Thr	His	275	280	285	
Thr	Glu	Leu	Ser	Ser	Ile	Leu	Thr	Ile	His	Asn	Val	Ser	Gln	His	Asp	290	295	300	
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Glu	Ser	Thr	Glu	Val	Ile	Val	His	Glu	Asn	Pro	Phe	Ile	Ser	Val	Glu	325	330	335	
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Lys	Leu	Pro	Val	Lys	Leu	Ala	Ala	Tyr	Pro	Pro	Pro	Glu	Phe	Gln	Trp	355	360	365	
Tyr	Lys	Asp	Gly	Lys	Ala	Leu	Ser	Gly	Arg	His	Ser	Pro	His	Ala	Leu	370	375	380	
Val	Leu	Lys	Glu	Val	Thr	Glu	Ala	Ser	Thr	Gly	Thr	Tyr	Thr	Leu	Ala	385	390	395	400
Leu	Trp	Asn	Ser	Ala	Ala	Gly	Leu	Arg	Arg	Asn	Ile	Ser	Leu	Glu	Leu	405	410	415	
Val	Val	Asn	Val	Pro	Pro	Gln	Ile	His	Glu	Lys	Glu	Ala	Ser	Ser	Pro	420	425	430	
Ser	Ile	Tyr	Ser	Arg	His	Ser	Arg	Gln	Ala	Leu	Thr	Cys	Thr	Ala	Tyr	435	440	445	

Gly	Val	Pro	Leu	Pro	Leu	Ser	Ile	Gln	Trp	His	Trp	Arg	Pro	Trp	Thr	450	455	460	
Pro	Cys	Lys	Met	Phe	Ala	Gln	Arg	Ser	Leu	Arg	Arg	Arg	Gln	Gln	Gln	465	470	475	480
Asp	Leu	Met	Pro	Gln	Cys	Arg	Asp	Trp	Arg	Ala	Val	Thr	Thr	Gln	Asp	485	490	495	
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Ser	Cys	Gln	Ala	Asp	Ser	Tyr	Lys	Tyr	Glu	His	Leu	Arg	Trp	Tyr	Arg	580	585	590	
Leu	Asn	Leu	Ser	Thr	Leu	His	Asp	Ala	His	Gly	Asn	Pro	Leu	Leu	Leu	595	600	605	
Asp	Cys	Lys	Asn	Val	His	Leu	Phe	Ala	Thr	Pro	Leu	Ala	Ala	Ser	Leu	610	615	620	
Glu	Glu	Val	Ala	Pro	Gly	Ala	Arg	His	Ala	Thr	Leu	Ser	Leu	Ser	Ile	625	630	635	640
Pro	Arg	Val	Ala	Pro	Glu	His	Glu	Gly	His	Tyr	Val	Cys	Glu	Val	Gln	645	650	655	
Asp	Arg	Arg	Ser	His	Asp	Lys	His	Cys	His	Lys	Lys	Tyr	Leu	Ser	Val	660	665	670	
Gln	Ala	Leu	Glu	Ala	Pro	Arg	Leu	Thr	Gln	Asn	Leu	Thr	Asp	Leu	Leu	675	680	685	
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His	Ala	Pro	Ser	Ile	Val	Trp	Tyr	Lys	Asp	Glu	Arg	Leu	Leu	Glu	Glu	705	710	715	720
Lys	Ser	Gly	Val	Asp	Leu	Ala	Asp	Ser	Asn	Gln	Lys	Leu	Ser	Ile	Gln	725	730	735	

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Leu	Lys	Glu	Gly	Ala	Thr	Ala	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	
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Lys	Val	Tyr	Thr	Thr	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	1090	1095	1100	
Trp	Glu	Ile	Phe	Ser	Leu	Gly	Ala	Ser	Pro	Tyr	Pro	Gly	Val	Gln	Ile	1105	1110	1115	1120
Asn	Glu	Glu	Phe	Cys	Gln	Arg	Leu	Arg	Asp	Gly	Thr	Arg	Met	Arg	Ala	1125	1130	1135	
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Gln	Val	Ser	Thr	Met	Ala	Leu	His	Ile	Ala	Gln	Ala	Asp	Ala	Glu	Asp	1205	1210	1215	
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tgg	ctc	tgc	ctg	gga	ctc	ctg	gac	ggc	ctg	gtg	agt	ggc	tac	tcc	atg	100
Trp	Leu	Cys	Leu	Gly	Leu	Leu	Asp	Gly	Leu	Val	Ser	Gly	Tyr	Ser	Met	
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Thr	Pro	Pro	Thr	Leu	Asn	Ile	Thr	Glu	Glu	Ser	His	Val	Ile	Asp	Thr	
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Gly	Asp	Ser	Leu	Ser	Ile	Ser	Cys	Arg	Gly	Gln	His	Pro	Leu	Glu	Trp	
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gct	tgg	cca	gga	gct	cag	gag	gcy	cca	gcc	acc	gga	gac	aag	gac	agc	244
Ala	Trp	Pro	Gly	Ala	Gln	Glu	Ala	Pro	Ala	Thr	Gly	Asp	Lys	Asp	Ser	
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Glu	Asp	Thr	Gly	Val	Val	Arg	Asp	Cys	Glu	Gly	Thr	Asp	Ala	Arg	Pro	
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tac	tgc	aag	gtg	ttg	ctg	ctg	cac	gag	gta	cat	gcc	aac	gac	aca	ggc	340
Tyr	Cys	Lys	Val	Leu	Leu	Leu	His	Glu	Val	His	Ala	Asn	Asp	Thr	Gly	
			95					100					105			
agc	tac	gtc	tgc	tac	tac	aag	tac	atc	aag	gca	cgc	atc	gag	ggc	acc	388
Ser	Tyr	Val	Cys	Tyr	Tyr	Lys	Tyr	Ile	Lys	Ala	Arg	Ile	Glu	Gly	Thr	
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acg	gcc	gcc	agc	tcc	tac	gtg	ttc	gtg	aga	gac	ttt	gag	cag	cca	ttc	436
Thr	Ala	Ala	Ser	Ser	Tyr	Val	Phe	Val	Arg	Asp	Phe	Glu	Gln	Pro	Phe	
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atc	aac	aag	cct	gac	acg	ctc	ttg	gtc	aac	agg	aag	gac	gcc	atg	tgg	484
Ile	Asn	Lys	Pro	Asp	Thr	Leu	Leu	Val	Asn	Arg	Lys	Asp	Ala	Met	Trp	
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Gln Ser Ser Val Leu Trp Pro Asp Gly Gln Glu Val Val Trp Asp Asp	
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Arg Arg Gly Met Leu Val Ser Thr Pro Leu Leu His Asp Ala Leu Tyr	
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Leu Gln Cys Glu Thr Thr Trp Gly Asp Gln Asp Phe Leu Ser Asn Pro	
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Phe Leu Val His Ile Thr Gly Asn Glu Leu Tyr Asp Ile Gln Leu Leu	
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Pro Arg Lys Ser Leu Glu Leu Leu Val Gly Glu Lys Leu Val Leu Asn	
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Cys Thr Val Trp Ala Glu Phe Asn Ser Gly Val Thr Phe Asp Trp Asp	
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Val Ser Gln His Asp Leu Gly Ser Tyr Val Cys Lys Ala Asn Asn Gly	
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Gly Asp Glu Leu Val Lys Leu Pro Val Lys Leu Ala Ala Tyr Pro Pro	
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Pro Glu Phe Gln Trp Tyr Lys Asp Gly Lys Ala Leu Ser Gly Arg His	
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Ser Pro His Ala Leu Val Leu Lys Glu Val Thr Glu Ala Ser Thr Gly	
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Thr Tyr Thr Leu Ala Leu Trp Asn Ser Ala Ala Gly Leu Arg Arg Asn	
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Trp Arg Pro Trp Thr Pro Cys Lys Met Phe Ala Gln Arg Ser Leu Arg	
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Gln Asn Ala Asn Val Ser Ala Met Tyr Lys Cys Val Val Ser Asn Lys	
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 agaggcagcc cgcacacctg cgctggggtg ttgagagcca tcctgcaagt ctttttc 4795

<210> 4
 <211> 1363
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Gln Arg Gly Ala Ala Leu Cys Leu Arg Leu Trp Leu Cys Leu Gly
 1 5 10 15
 Leu Leu Asp Gly Leu Val Ser Gly Tyr Ser Met Thr Pro Pro Thr Leu
 20 25 30
 Asn Ile Thr Glu Glu Ser His Val Ile Asp Thr Gly Asp Ser Leu Ser
 35 40 45
 Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Ala Trp Pro Gly Ala
 50 55 60
 Gln Glu Ala Pro Ala Thr Gly Asp Lys Asp Ser Glu Asp Thr Gly Val
 65 70 75 80
 Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro Tyr Cys Lys Val Leu
 85 90 95
 Leu Leu His Glu Val His Ala Asn Asp Thr Gly Ser Tyr Val Cys Tyr
 100 105 110
 Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr Thr Ala Ala Ser Ser
 115 120 125
 Tyr Val Phe Val Arg Asp Phe Glu Gln Pro Phe Ile Asn Lys Pro Asp
 130 135 140
 Thr Leu Leu Val Asn Arg Lys Asp Ala Met Trp Val Pro Cys Leu Val
 145 150 155 160
 Ser Ile Pro Gly Leu Asn Val Thr Leu Arg Ser Gln Ser Ser Val Leu
 165 170 175
 Trp Pro Asp Gly Gln Glu Val Val Trp Asp Asp Arg Arg Gly Met Leu
 180 185 190
 Val Ser Thr Pro Leu Leu His Asp Ala Leu Tyr Leu Gln Cys Glu Thr
 195 200 205

Thr	Trp	Gly	Asp	Gln	Asp	Phe	Leu	Ser	Asn	Pro	Phe	Leu	Val	His	Ile
210						215					220				
Thr	Gly	Asn	Glu	Leu	Tyr	Asp	Ile	Gln	Leu	Leu	Pro	Arg	Lys	Ser	Leu
225					230					235					240
Glu	Leu	Leu	Val	Gly	Glu	Lys	Leu	Val	Leu	Asn	Cys	Thr	Val	Trp	Ala
				245					250					255	
Glu	Phe	Asn	Ser	Gly	Val	Thr	Phe	Asp	Trp	Asp	Tyr	Pro	Gly	Lys	Gln
			260					265					270		
Ala	Glu	Arg	Gly	Lys	Trp	Val	Pro	Glu	Arg	Arg	Ser	Gln	Gln	Thr	His
		275					280					285			
Thr	Glu	Leu	Ser	Ser	Ile	Leu	Thr	Ile	His	Asn	Val	Ser	Gln	His	Asp
290						295					300				
Leu	Gly	Ser	Tyr	Val	Cys	Lys	Ala	Asn	Asn	Gly	Ile	Gln	Arg	Phe	Arg
305					310					315					320
Glu	Ser	Thr	Glu	Val	Ile	Val	His	Glu	Asn	Pro	Phe	Ile	Ser	Val	Glu
				325					330					335	
Trp	Leu	Lys	Gly	Pro	Ile	Leu	Glu	Ala	Thr	Ala	Gly	Asp	Glu	Leu	Val
			340					345					350		
Lys	Leu	Pro	Val	Lys	Leu	Ala	Ala	Tyr	Pro	Pro	Pro	Glu	Phe	Gln	Trp
		355					360					365			
Tyr	Lys	Asp	Gly	Lys	Ala	Leu	Ser	Gly	Arg	His	Ser	Pro	His	Ala	Leu
	370					375					380				
Val	Leu	Lys	Glu	Val	Thr	Glu	Ala	Ser	Thr	Gly	Thr	Tyr	Thr	Leu	Ala
385					390					395					400
Leu	Trp	Asn	Ser	Ala	Ala	Gly	Leu	Arg	Arg	Asn	Ile	Ser	Leu	Glu	Leu
				405					410					415	
Val	Val	Asn	Val	Pro	Pro	Gln	Ile	His	Glu	Lys	Glu	Ala	Ser	Ser	Pro
			420					425					430		
Ser	Ile	Tyr	Ser	Arg	His	Ser	Arg	Gln	Ala	Leu	Thr	Cys	Thr	Ala	Tyr
		435					440					445			
Gly	Val	Pro	Leu	Pro	Leu	Ser	Ile	Gln	Trp	His	Trp	Arg	Pro	Trp	Thr
	450					455					460				
Pro	Cys	Lys	Met	Phe	Ala	Gln	Arg	Ser	Leu	Arg	Arg	Arg	Gln	Gln	Gln
465					470					475					480
Asp	Leu	Met	Pro	Gln	Cys	Arg	Asp	Trp	Arg	Ala	Val	Thr	Thr	Gln	Asp
				485					490					495	

Ala	Val	Asn	Pro	Ile	Glu	Ser	Leu	Asp	Thr	Trp	Thr	Glu	Phe	Val	Glu
500						505			510						
Gly	Lys	Asn	Lys	Thr	Val	Ser	Lys	Leu	Val	Ile	Gln	Asn	Ala	Asn	Val
515						520			525						
Ser	Ala	Met	Tyr	Lys	Cys	Val	Val	Ser	Asn	Lys	Val	Gly	Gln	Asp	Glu
530						535			540						
Arg	Leu	Ile	Tyr	Phe	Tyr	Val	Thr	Thr	Ile	Pro	Asp	Gly	Phe	Thr	Ile
545			550						555			560			
Glu	Ser	Lys	Pro	Ser	Glu	Glu	Leu	Leu	Glu	Gly	Gln	Pro	Val	Leu	Leu
			565						570			575			
Ser	Cys	Gln	Ala	Asp	Ser	Tyr	Lys	Tyr	Glu	His	Leu	Arg	Trp	Tyr	Arg
			580			585			590						
Leu	Asn	Leu	Ser	Thr	Leu	His	Asp	Ala	His	Gly	Asn	Pro	Leu	Leu	Leu
595						600			605						
Asp	Cys	Lys	Asn	Val	His	Leu	Phe	Ala	Thr	Pro	Leu	Ala	Ala	Ser	Leu
610						615			620						
Glu	Glu	Val	Ala	Pro	Gly	Ala	Arg	His	Ala	Thr	Leu	Ser	Leu	Ser	Ile
625			630						635			640			
Pro	Arg	Val	Ala	Pro	Glu	His	Glu	Gly	His	Tyr	Val	Cys	Glu	Val	Gln
			645						650			655			
Asp	Arg	Arg	Ser	His	Asp	Lys	His	Cys	His	Lys	Lys	Tyr	Leu	Ser	Val
			660			665			670						
Gln	Ala	Leu	Glu	Ala	Pro	Arg	Leu	Thr	Gln	Asn	Leu	Thr	Asp	Leu	Leu
675						680			685						
Val	Asn	Val	Ser	Asp	Ser	Leu	Glu	Met	Gln	Cys	Leu	Val	Ala	Gly	Ala
690						695			700						
His	Ala	Pro	Ser	Ile	Val	Trp	Tyr	Lys	Asp	Glu	Arg	Leu	Leu	Glu	Glu
705			710						715			720			
Lys	Ser	Gly	Val	Asp	Leu	Ala	Asp	Ser	Asn	Gln	Lys	Leu	Ser	Ile	Gln
			725						730			735			
Arg	Val	Arg	Glu	Glu	Asp	Ala	Gly	Arg	Tyr	Leu	Cys	Ser	Val	Cys	Asn
			740			745			750						
Ala	Lys	Gly	Cys	Val	Asn	Ser	Ser	Ala	Ser	Val	Ala	Val	Glu	Gly	Ser
755						760			765						
Glu	Asp	Lys	Gly	Ser	Met	Glu	Ile	Val	Ile	Leu	Val	Gly	Thr	Gly	Val
770			775						780						

Ile	Ala	Val	Phe	Phe	Trp	Val	Leu	Leu	Leu	Leu	Ile	Phe	Cys	Asn	Met	785	790	795	800
Arg	Arg	Pro	Ala	His	Ala	Asp	Ile	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Ile	805	810	815	
Met	Asp	Pro	Gly	Glu	Val	Pro	Leu	Glu	Glu	Gln	Cys	Glu	Tyr	Leu	Ser	820	825	830	
Tyr	Asp	Ala	Ser	Gln	Trp	Glu	Phe	Pro	Arg	Glu	Arg	Leu	His	Leu	Gly	835	840	845	
Arg	Val	Leu	Gly	Tyr	Gly	Ala	Phe	Gly	Lys	Val	Val	Glu	Ala	Ser	Ala	850	855	860	
Phe	Gly	Ile	His	Lys	Gly	Ser	Ser	Cys	Asp	Thr	Val	Ala	Val	Lys	Met	865	870	875	880
Leu	Lys	Glu	Gly	Ala	Thr	Ala	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	885	890	895	
Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	Asn	His	Leu	Asn	Val	Val	Asn	Leu	900	905	910	
Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gln	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	915	920	925	
Phe	Cys	Lys	Tyr	Gly	Asn	Leu	Ser	Asn	Phe	Leu	Arg	Ala	Lys	Arg	Asp	930	935	940	
Ala	Phe	Ser	Pro	Cys	Ala	Glu	Lys	Ser	Pro	Glu	Gln	Arg	Gly	Arg	Phe	945	950	955	960
Arg	Ala	Met	Val	Glu	Leu	Ala	Arg	Leu	Asp	Arg	Arg	Arg	Pro	Gly	Ser	965	970	975	
Ser	Asp	Arg	Val	Leu	Phe	Ala	Arg	Phe	Ser	Lys	Thr	Glu	Gly	Gly	Ala	980	985	990	
Arg	Arg	Ala	Ser	Pro	Asp	Gln	Glu	Ala	Glu	Asp	Leu	Trp	Leu	Ser	Pro	995	1000	1005	
Leu	Thr	Met	Glu	Asp	Leu	Val	Cys	Tyr	Ser	Phe	Gln	Val	Ala	Arg	Gly	1010	1015	1020	
Met	Glu	Phe	Leu	Ala	Ser	Arg	Lys	Cys	Ile	His	Arg	Asp	Leu	Ala	Ala	1025	1030	1035	1040
Arg	Asn	Ile	Leu	Leu	Ser	Glu	Ser	Asp	Val	Val	Lys	Ile	Cys	Asp	Phe	1045	1050	1055	
Gly	Leu	Ala	Arg	Asp	Ile	Tyr	Lys	Asp	Pro	Asp	Tyr	Val	Arg	Lys	Gly	1060	1065	1070	

Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp		
1075	1080	1085
Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu		
1090	1095	1100
Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile		
1105	1110	1115 1120
Asn Glu Glu Phe Cys Gln Arg Leu Arg Asp Gly Thr Arg Met Arg Ala		
1125	1130	1135
Pro Glu Leu Ala Thr Pro Ala Ile Arg Arg Ile Met Leu Asn Cys Trp		
1140	1145	1150
Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Glu Leu Val Glu Ile		
1155	1160	1165
Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln Glu Glu Glu Glu Val		
1170	1175	1180
Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser		
1185	1190	1195 1200
Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp		
1205	1210	1215
Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn		
1220	1225	1230
Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly		
1235	1240	1245
Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr		
1250	1255	1260
Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala		
1265	1270	1275 1280
Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly		
1285	1290	1295
Phe Ser Cys Lys Gly Pro Gly Gln Asn Val Ala Val Thr Arg Ala His		
1300	1305	1310
Pro Asp Ser Gln Gly Arg Arg Arg Arg Pro Glu Arg Gly Ala Arg Gly		
1315	1320	1325
Gly Gln Val Phe Tyr Asn Ser Glu Tyr Gly Glu Leu Ser Glu Pro Ser		
1330	1335	1340

Glu Glu Asp His Cys Ser Pro Ser Ala Arg Val Thr Phe Phe Thr Asp
345 1350 1355 1360

Asn Ser Tyr

<210> 5

<211> 1311

<212> PRT

<213> Homo sapiens (FLT1)

<400> 5

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
20 25 30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
50 55 60

Glu Asn Asn Asn Asn Asn Asn Met Val Ser Lys Glu Ser Glu Arg Leu
65 70 75 80

Ser Ile Thr Lys Ser Ala Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser
85 90 95

Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn His Thr Gly Phe Tyr Ser
100 105 110

Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser
115 120 125

Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met
130 135 140

Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu
145 150 155 160

Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys
165 170 175

Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp
180 185 190

Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile
195 200 205

Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr
210 215 220

Asn	Asn	Tyr	Leu	Thr	His	Arg	Gln	Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln	225	230	235	240
Ile	Ser	Thr	Pro	Arg	Pro	Val	Lys	Leu	Leu	Arg	Gly	His	Thr	Leu	Val	245	250	255	
Leu	Asn	Cys	Thr	Ala	Thr	Thr	Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr	260	265	270	
Trp	Ser	Tyr	Pro	Asp	Asn	Asn	Asn	Glu	Lys	Asn	Lys	Arg	Ala	Ser	Val	275	280	285	
Arg	Arg	Arg	Ile	Asp	Gln	Ser	Asn	Ser	His	Ala	Asn	Ile	Phe	Tyr	Ser	290	295	300	
Val	Leu	Thr	Ile	Asp	Lys	Met	Gln	Asn	Lys	Asp	Lys	Gly	Leu	Tyr	Thr	305	310	315	320
Cys	Arg	Val	Arg	Ser	Gly	Pro	Ser	Phe	Lys	Ser	Val	Asn	Thr	Ser	Val	325	330	335	
His	Ile	Tyr	Asp	Lys	Ala	Phe	Ile	Thr	Val	Lys	His	Arg	Lys	Gln	Gln	340	345	350	
Val	Leu	Glu	Thr	Val	Ala	Gly	Lys	Arg	Ser	Tyr	Arg	Leu	Ser	Met	Lys	355	360	365	
Val	Lys	Ala	Phe	Pro	Ser	Pro	Glu	Val	Val	Trp	Leu	Lys	Asp	Gly	Leu	370	375	380	
Pro	Ala	Thr	Glu	Lys	Ser	Ala	Arg	Tyr	Leu	Thr	Arg	Gly	Tyr	Ser	Leu	385	390	395	400
Ile	Ile	Lys	Asp	Val	Thr	Glu	Glu	Asp	Ala	Gly	Asn	Tyr	Thr	Ile	Leu	405	410	415	
Leu	Ser	Ile	Lys	Gln	Ser	Asn	Val	Phe	Lys	Asn	Leu	Thr	Ala	Thr	Leu	420	425	430	
Ile	Val	Asn	Val	Lys	Pro	Gln	Ile	Tyr	Glu	Lys	Ala	Val	Ser	Ser	Phe	435	440	445	
Pro	Asp	Pro	Ala	Leu	Tyr	Pro	Leu	Gly	Ser	Arg	Gln	Ile	Leu	Thr	Cys	450	455	460	
Thr	Ala	Tyr	Gly	Ile	Pro	Gln	Pro	Asn	Thr	Ile	Lys	Trp	Phe	Trp	His	465	470	475	480
Pro	Cys	Asn	His	Asn	His	Ser	Glu	Ala	Arg	Cys	Asp	Phe	Cys	Ser	Asn	485	490	495	
Asn	Glu	Glu	Ser	Phe	Ile	Leu	Asp	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Ala	500	505	510	

Asp	Ser	Asn	Met	Gly	Asn	Arg	Ile	Glu	Ser	Ile	Thr	Gln	Arg	Met	Ala	
		515					520					525				
Ile	Ile	Glu	Gly	Lys	Asn	Lys	Met	Ala	Ser	Thr	Leu	Val	Val	Ala	Asp	
		530				535					540					
Ser	Arg	Ile	Ser	Gly	Ile	Tyr	Ile	Cys	Ile	Ala	Ser	Asn	Lys	Val	Gly	
545					550					555					560	
Thr	Val	Gly	Arg	Asn	Ile	Ser	Phe	Tyr	Ile	Thr	Asp	Val	Pro	Asn	Gly	
				565					570					575		
Phe	His	Val	Asn	Leu	Glu	Lys	Met	Pro	Thr	Asn	Asn	Glu	Gly	Glu	Asp	
			580					585					590			
Leu	Lys	Leu	Ser	Cys	Thr	Val	Asn	Lys	Phe	Leu	Tyr	Arg	Asp	Val	Thr	
		595					600					605				
Trp	Ile	Leu	Leu	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	
610						615						620				
Asn	Asn	Asn	Asn	Asn	Arg	Thr	Val	Asn	Asn	Arg	Thr	Met	His	Tyr	Ser	
625					630					635					640	
Ile	Ser	Lys	Gln	Lys	Met	Ala	Ile	Thr	Lys	Glu	His	Ser	Ile	Thr	Leu	
				645					650						655	
Asn	Leu	Thr	Ile	Met	Asn	Val	Ser	Leu	Gln	Asp	Ser	Gly	Thr	Tyr	Ala	
			660					665						670		
Cys	Arg	Ala	Arg	Asn	Val	Tyr	Thr	Gly	Glu	Glu	Ile	Leu	Gln	Lys	Lys	
		675					680					685				
Glu	Ile	Thr	Ile	Arg	Asp	Gln	Glu	Ala	Pro	Tyr	Leu	Leu	Arg	Asn	Leu	
		690				695					700					
Ser	Asp	His	Thr	Val	Ala	Ile	Ser	Ser	Ser	Thr	Thr	Leu	Asp	Cys	His	
705					710					715					720	
Ala	Asn	Gly	Val	Pro	Glu	Pro	Gln	Ile	Thr	Trp	Phe	Lys	Asn	Asn	His	
				725					730					735		
Lys	Ile	Gln	Gln	Glu	Pro	Gly	Ile	Ile	Leu	Gly	Pro	Gly	Ser	Ser	Thr	
			740					745					750			
Leu	Phe	Ile	Glu	Arg	Val	Thr	Glu	Glu	Asp	Glu	Gly	Val	Tyr	His	Cys	
		755					760					765				
Lys	Ala	Thr	Asn	Gln	Lys	Gly	Ser	Val	Glu	Ser	Ser	Ala	Tyr	Leu	Thr	
		770				775					780					
Val	Gln	Gly	Thr	Ser	Asp	Lys	Ser	Asn	Leu	Glu	Leu	Ile	Thr	Leu	Thr	
785					790					795					800	

Cys Thr Cys Val	Ala Ala Thr Leu Phe Trp Leu Leu Leu Thr Leu Leu	805	810	815
Ile Arg Lys Met	Lys Arg Ser Ser Asn Ser Glu Ile Lys Thr Asp Tyr	820	825	830
Leu Ser Ile Ile	Met Asp Pro Asp Glu Val Pro Leu Asp Glu Gln Cys	835	840	845
Glu Arg Leu Pro	Tyr Asp Ala Ser Lys Trp Glu Phe Ala Arg Glu Arg	850	855	860
Leu Lys Leu Gly	Lys Ser Leu Gly Arg Gly Ala Phe Gly Lys Val Val	865	870	875
Gln Ala Ser Ala	Phe Gly Ile Lys Lys Ser Pro Thr Cys Arg Thr Val	885	890	895
Ala Val Lys Met	Leu Lys Glu Gly Ala Thr Ala Ser Glu Tyr Lys Ala	900	905	910
Leu Met Thr Glu	Leu Lys Ile Leu Thr His Ile Gly His His Leu Asn	915	920	925
Val Val Asn Leu	Leu Gly Ala Cys Thr Lys Gln Gly Gly Pro Leu Met	930	935	940
Val Ile Val Glu	Tyr Cys Lys Tyr Gly Asn Leu Ser Asn Tyr Leu Lys	945	950	955
Ser Lys Arg Asp	Leu Phe Phe Leu Asn Lys Asp Ala Ala Leu His Met	965	970	975
Glu Pro Lys Lys	Glu Lys Met Glu Pro Gly Leu Glu Gln Gly Lys Lys	980	985	990
Pro Arg Leu Asp	Ser Val Thr Ser Ser Glu Ser Phe Ala Ser Ser Gly	995	1000	1005
Phe Gln Glu Asp	Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Asp Ser	1010	1015	1020
Asp Gly Phe Tyr	Lys Glu Pro Ile Thr Met Glu Asp Leu Ile Ser Tyr	1025	1030	1035
Ser Phe Gln Val	Ala Arg Gly Met Glu Phe Leu Ser Ser Arg Lys Cys	1045	1050	1055
Ile His Arg Asp	Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Asn Asn	1060	1065	1070
Val Val Lys Ile	Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asn	1075	1080	1085

- 111 -

Pro Asp Tyr Val Arg Lys Gly Asp Thr Arg Leu Pro Leu Lys Trp Met
1090 1095 1100

Ala Pro Glu Ser Ile Phe Asp Lys Ile Tyr Ser Thr Lys Ser Asp Val
1105 1110 1115 1120

Trp Ser Tyr Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Ser
1125 1130 1135

Pro Tyr Pro Gly Val Gln Met Asp Glu Asp Phe Cys Ser Arg Leu Arg
1140 1145 1150

Glu Gly Met Arg Met Arg Ala Pro Glu Tyr Ser Thr Pro Glu Ile Tyr
1155 1160 1165

Gln Ile Met Leu Asp Cys Trp His Arg Asp Pro Lys Glu Arg Pro Arg
1170 1175 1180

Phe Ala Glu Leu Val Glu Lys Leu Gly Asp Leu Leu Gln Ala Asn Val
1185 1190 1195 1200

Gln Gln Asp Gly Lys Asp Tyr Ile Pro Ile Asn Ala Ile Leu Thr Gly
1205 1210 1215

Asn Ser Gly Phe Thr Tyr Ser Thr Pro Ala Phe Ser Glu Asp Phe Phe
1220 1225 1230

Lys Glu Ser Ile Ser Ala Pro Lys Phe Asn Ser Gly Ser Ser Asp Asp
1235 1240 1245

Val Arg Tyr Val Asn Ala Phe Lys Phe Met Ser Leu Glu Arg Ile Lys
1250 1255 1260

Thr Phe Glu Glu Leu Leu Pro Asn Ala Thr Ser Met Phe Asp Asp Tyr
1265 1270 1275 1280

Gln Gly Asp Ser Ser Thr Leu Leu Ala Ser Pro Met Leu Lys Arg Phe
1285 1290 1295

Thr Trp Thr Asp Ser Lys Pro Lys Ala Ser Leu Lys Ile Glu Val
1300 1305 1310

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> The amino acid at positions 1 and 2 each are
selected independently from the group consisting
of aspartic acid and glutamic acid.

<220>

<223> The amino acid at position 4 is independently selected from the group consisting of methionine and valine.

<220>

<223> The amino acid at position 5 is independently selected from the group consisting of proline, aspartic acid, and glutamic acid.

<220>

<223> Description of Artificial Sequence: consensus sequence

<400> 6

Xaa Xaa Tyr Xaa Xaa Met
1 5

<210> 7

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide probe

<400> 7

acatgcatgc caccatgcag cggggcgccg cgctgtgcct gcgactgtgg ctctgcctgg 60
gactcctgga 70

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide probe

<400> 8

acatgcatgc cccgccggtc atcc 24

<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide probe

<400> 9
cggaattccc catgacccca ac 22

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 10
ccatcgatgg atcctacctg aagccgcttt ctt 33

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 11
cccaagcttg gatccaagtg gctactccat gacc 34

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 12
gttgctgtg atgtgcacca 20

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 13
ctggagtcga cttggcggac t

21

<210> 14
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 14
cgcggtatccc tagtgatggt gatggtgatg tctaccttcg atcatgctgc ccttatcctc 60

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 15
ctggagtcga cttggcggac t

21

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 16
cgggatccct ccatgctgcc cttatcct

28

<210> 17
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 17
ggcaagcttg aattcgccac catgcagcgg ggcgcc 36

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 18
gttgctgtg atgtgcacca 20

<210> 19
<211> 21
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 19
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<223> Description of Artificial Sequence:
oligonucleotide probe

<400> 20
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<213> Homo sapiens

<400> 21
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Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
 35 40 45
 Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
 50 55 60
 Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
 65 70 75 80
 Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
 85 90 95
 Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
 100 105 110
 His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
 115 120 125
 Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
 130 135 140
 Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
 145 150 155 160
 Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
 165 170 175
 Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
 180 185 190
 Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
 195 200 205
 Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
 210 215 220
 Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
 225 230 235 240
 Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
 245 250 255
 Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
 260 265 270
 Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
 275 280 285
 Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
 290 295 300
 Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
 305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
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Gln Met Ser

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<211> 354

<212> PRT

<213> Homo sapiens

<400> 22

Met Tyr Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val
1 5 10 15

Gln Leu Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser
20 25 30

Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
35 40 45

Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
50 55 60

Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100 105 110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115 120 125

[illegible]